## REMARKS

Sequence Listing

The Examiner required a new paper copy and computer readable form (CRF) of the Sequence Listing. Action at page 2. Applicants enclose a new paper copy of the Sequence Listing and an amended substitute copy of the CRF of the Sequence Listing. The undersigned states that the information contained in the CRF of the Sequence Listing is identical to the Paper Copy of the Sequence Listing (30 pages), and that the Sequence Listing adds no new matter.

Status of the Claims

Claims 1-38 have been cancelled without prejudice or disclaimer. New claims 39-58 have been added. The new claims correspond to the subject matter of the cancelled claims and are supported in the specification as described previously for the cancelled claims and as set forth below. It is believed that no new matter has been introduced and no issues regarding further consideration and/or search by the Examiner have been raised. Entry of the new claims is respectfully requested.

New claims 39-41, 44, 46, 47 and 49-51 recite, "at least one activity selected from a T-cell proliferation activity, a T-cell activation activity, and a binding activity to CRP1." Support for these recitations can be found in original claims 2, 33, 34, 36, and 37, and in the specification, for example, at page 41, line 32 to page 42, line 6.

New claims 41 and 45 recite, "a nucleotide sequence encoding a polypeptide ... as set forth in Figure 12A (SEQ ID NO: 17) from residues 1-302, or from about residues 19-302, 20-302, 21-302, 22-302, 24-302, or 28-302." New claim 49 recites a nucleotide sequence "encoding an extracellular domain of B7RP1 as set forth in Figure 12 A (SEQ ID NO: 17), or a fragment thereof." Support for the new claims can be found in original claim 2, and in the specification, for example, at page 22, lines 17-31, and at page 40, line 27 to page 41, line 8.

References to SEQ ID NOs: 1 and 2, which are non-elected sequences, no longer appear in the new claims.

Claims 40, 42 and 44 now recite "wherein the nucleotide sequence is not the nucleotide sequence of GenBank Accession No. AB014533". Claims 49-51 now recite "wherein the nucleotide sequence is not the nucleotide sequence of GenBank Accession No. AB014533 or GenBank Accession No. R23544". Both GenBank entries were cited as prior art by the Examiner and, as such, need not be explicitly supported in the specification. Nonetheless, support for "GenBank Accession No. AB104533" is found at p. 72, line 25 of the specification.

Applicant notes that the disclaimers recited in Claims 40, 42, 44 are intended solely to exclude the specific nucleotide sequence present in GenBank Accession No. AB104533 while those in Claims 49-51 are intended solely to exclude the specific nucleotide sequences present in GenBank Accession No. AB104533 and GenBank Accession No. R23544. Such disclaimers in no way limit or are prejudicial to the scope of any pending claims in the present application, or claims issuing thereon, nor do they limit Applicant's rights to pursue claims to additional nucleotide sequences in subsequent continuation, continuation-in-part or divisional applications.

Claim 47 (corresponding to original claim 37) no longer recites the term "about" prior to the language "residue 302."

Rejections Under 35 U.S.C. § 112, second paragraph

The Examiner rejected claims 2-7, 32-34, and 36-37 under 35 U.S.C. § 112, second paragraph, for allegedly "failing to particularly point out and distinctly claim the subject matter which the applicant regards as the invention." Action at page 3. Applicants respectfully traverse this rejection. The Examiner discussed certain terms used in the claims which will be addressed in turn.

A) "B7RP1"

The Examiner alleged that claims 2-7, 32-34, and 36-37 are "indefinite in that they recite an arbitrary protein name, 'B7RP1'." Action at page 3. According to the Examiner, "B7RP1" can be distinctly claimed "by claiming a sufficient number of characteristics associated with the protein (e.g., activity and amino acid composition, etc.)" *Id.*

Applicants respectfully traverse. Solely to expedite prosecution and without acquiescing to any rejection, Applicants have added new claims 39-41, 44, 46, 47 and 49-51 which recite "wherein the polypeptide [or polypeptide fragment] has at least one activity selected from a T-cell proliferation activity, a T-cell activation activity, and a binding activity to CRP1." Applicants assert that the specification teaches several sequences for each of CRP1 and B7RP1 and describes the structure of both proteins in detail at least at page 20, line 19, to page 23, line 4. Furthermore, the proposed claim amendments make clear what activity is associated with the "CRP1" or "B7RP1" proteins. Applicants therefore assert that claims 2-7, 32-34, and 36-37 are not indefinite in their recitation of "B7RP1."

B) "At least one activity characteristic" of B7RP1

The Examiner rejected claims 2-7, 33-34, and 36-37 as allegedly being "indefinite in their recitation of polypeptides and polypeptide fragments having 'at least one activity characteristic' of B7RP1." Action at page 3. The Examiner admitted that the specification discloses that "binding to a CRP1 polypeptide and the ability to stimulate T cell proliferation and/or activation are activities which are characteristic of a B7RP1 polypeptide." *Id.* However, the Examiner alleged that two disclosed B7RP1 activities do not "establish the metes and bound [sic] of what constitutes an 'activity characteristic' of B7RP1." *Id.*

Applicants respectfully traverse this basis for the rejection. Solely to expedite prosecution and without acquiescing to any rejection, Applicants have added new claims 39-41, 44, 46, 47 and 49-51 which recite "wherein the polypeptide [or polypeptide fragment] has at least one activity selected from a T-cell proliferation activity, a T-cell activation activity, and a binding activity to CRP1." Applicants assert that this basis for the § 112, second paragraph, rejection is therefore moot.

C) "High stringency conditions"

The Examiner rejected claims 2-7, and 32-33 as allegedly being indefinite in their recitation of "high stringency conditions." The Examiner admitted that the specification discloses "general parameters for calculating such conditions and examples of such conditions." Action at page 3. The Examiner maintained, however, that in the absence of a clear definition of the phrase, the exact conditions being claimed are unclear.

Applicants respectfully traverse this basis for the rejection. Solely to expedite prosecution and without acquiescing to any rejection, Applicants have added new claims in which the hybridization language is removed. Applicants therefore assert that this basis for the § 112, second paragraph, rejection is moot.

Applicants respectfully request reconsideration and withdrawal of the § 112, second paragraph, rejection.

Rejections Under 35 U.S.C. § 112, first paragraph (written description)

The examiner rejected claims 2-7 and 34 under 35 U.S.C. § 112, first paragraph, as allegedly "containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention." Action at page 4. Applicants respectfully traverse this rejection. The Examiner discussed certain terms used in the claims which will be addressed in turn.

A) "Percent Identity Variants"

The Examiner rejected certain claims that "recite a genus of nucleic acids but do not require that the polypeptides encoded by the instant nucleic acids share any testable functional activity, a feature deemed essential to the instant invention." Action at page 4. Specifically, the Examiner argued that "there does not appear to be an adequate written description in the specification as filed as to a *correlation*

between the structures encompassed by 70% identity or variants of the recited sequence and any *particular* function." Action at page 5 (emphasis original).

Applicants respectfully traverse this rejection and incorporate by reference the arguments made at pages 15-17 of the Amendment and Response filed May 5, 2003. Solely to expedite prosecution and without acquiescing to any rejection, Applicants have added new claims that do not recite percent identity language and have added new Claim 51 which recites "at least about 95 percent identical," and "at least one activity selected from a T-cell proliferation activity, a T-cell activation activity, and a binding activity to CRP1."

Applicants assert that the specification describes the nucleotide and amino acid sequences of both murine and human B7RP1 at least at SEQ ID NOs: 6, 7, 11, 12, 16, and 17 (*see* Figures 2A, 3A, and 12A). Polypeptides that are at least 95% identical to a polypeptide having a particular sequence identification number recited in claim 51 are specifically structurally related to such sequences. Moreover, the specification describes a T-cell proliferation assay at Example 17, an in vitro T-cell stimulation assay at Example 21, and a binding assay between a CRP1 and a B7RP1 protein at Example 8. Therefore, adequate structure and function is provided and the claimed invention is adequately described.

Thus, the Examiner has failed to establish Applicants' failure to comply with the written description requirement of § 112, first paragraph.

B) "Fragments"

The Examiner rejected certain claims alleging that "[f]ragment language that encompasses open (comprising) claim language permits unidentified flanking sequence to be added any [sic] subsequence of a particular SEQ ID NO and so does not allow one skilled in the art to visualize or recognize the identity of the subject matter purportedly described." Action at page 5. The Examiner admitted that for such a claim to be allowable, it is not necessary that every possible flanking sequence be described, and that the "comprising" language in and of itself does not render such a claim unpatentable. *Id.* The Examiner's

concern appears to be that the cited language encompasses a large genus of polypeptides and does not impose a correlation between the structure of the genus and a testable function. *Id.*

Applicants respectfully traverse this rejection and incorporate by reference the arguments made at page 17-18 of the Amendment and Response filed May 5, 2003. Solely to expedite prosecution and without acquiescing to any rejection, Applicants have added new claims 49-51 which recite the language, "wherein the fragment has at least one activity selected from a T-cell proliferation activity, a T-cell activation activity, and a binding activity to CRP1." Applicants assert that the specification describes how to make a polypeptide containing a fragment of one of the polypeptide sequences of the invention (*see*, e.g., the B7RP1-Fc fusion protein construct described at page 29, line 27, to page 30, line 2, and Example 7). Moreover, the specification describes a T-cell proliferation assay at Example 17, an in vitro T-cell stimulation assay at Example 21, and a binding assay between CRP1 and B7RP1 at Example 8. Thus, adequate structure and function are provided by the specification and the claimed invention is adequately described.

Thus, the Examiner has failed to establish that there is insufficient written description for claims containing the language "polypeptides comprising fragments."

C) "Hybridizes Under High Stringency Conditions"

The Examiner rejected certain claims alleging that "[t]he genus of nucleic acids which hybridizes to SEQ ID NOS: 6, 11 or 16, hybridize to nucleic acids comprising fragments thereof, or hybridize to nucleic acids encoding polypeptides at least about 70% identical is very large and a great deal of variability is encompassed by the instant claims." Action at page 6. The rejection appears to be specifically based on the premise that "an activity 'characteristic of B7RP1'... does not provide any particular function with which any aspect to the structure can be correlated," and that "the claims do not require that the hybridizing nucleic acids hybridize under any particular set of conditions." *Id.*

Applicants respectfully traverse this rejection. Solely to expedite prosecution and without acquiescing to any rejection, Applicants have added new claims which do not recite hybridization language.

Thus, the Examiner has failed to establish Applicants' failure to comply with the written description requirement of § 112, first paragraph.

D) An amino terminus "at about residue 1, 19, 20, 21, 22, 24 or 28.

The Examiner has rejected claim 36 for the recitation of "at about residue 1, 19, 20, 21, 22, 24, or 28." Action at page 10. Written support in the specification is found at p. 22, lines 19-22 which states that the leader sequence of B7RP1 shown in Figure 3A "encompasses about residues 1-18, 1-19, 1-20, 1-21, 1-23 or 1-27". It is apparent that such a description means that the amino terminus is at about residue 1, 19, 20, 21, 22, 24 or 28. Withdrawal of the rejection is requested.

E) "A Carboxy Terminus at about Residue 302"

The Examiner rejected claim 37 for the recitation of "at about residue 302." Action at page 10. Solely to expedite prosecution and not acquiescing to the rejection, Applicants have add new claim 47 which reads "at residue 302." The instant rejection is therefore moot with regard to these claims.

Applicants respectfully request reconsideration and withdrawal of the § 112, first paragraph, rejection based on the written description requirement.

Rejections Under 35 U.S.C. § 112, first paragraph (enablement)

The Examiner rejected claims 2-7 and 34 under 35 U.S.C. § 112, first paragraph, alleging that those claims were not reasonably enabled by the specification. See Action at page 7. The Examiner discussed certain terms used in the claims which will be addressed in turn.

A) "Encoding Variant Polypeptides"

The Examiner alleged that "the experimentation left to those skilled in the art to determine which 'variant' sequences would still encode polypeptides having the same function as the human and mouse B7-RP1 polypeptides disclosed in the specification as filed is unnecessarily, and improperly, extensive and undue." Action at page 8. The Examiner stated that "the skilled artisan would not reasonably expect such 'variant' polypeptides to have the same function as the instantly recited SEQ ID NOS, particularly when the family of B7-like proteins was known to have variable function." *Id.*, at page 7. The Examiner further stated that in the "absence of guidance as to which amino acid residues provide a particular function, it is unpredictable which, if any, sequences having 70% identity would maintain that function." *Id.*, at page 8.

Applicants respectfully traverse this rejection and incorporate by reference the arguments made at pages 19-20 of the Amendment and Response filed May 5, 2003. Solely to expedite prosecution and without acquiescing to any rejection, Applicants have added new claims 49-51 which recite "at least about 95 percent identical," and also recite "at least one activity selected from a T-cell proliferation activity, a T-cell activation activity, and a binding activity to CRP1."

Applicants submit that given the recitation of SEQ ID NOs: 7 and 17, and the teachings of the specification, one skilled in the art would have been able to isolate and identify nucleic acid molecules encoding polypeptide fragments having at least 95% identity to the polypeptides of SEQ ID NO: 7 and 17, and which have one or more of a T-cell proliferation activity, a T-cell activating activity, and a binding activity to CRP1. Furthermore, as discussed previously, the specification explicitly teaches appropriate assays for use in determining such protein activities at least at Examples 8, 17, and 21. Applicants maintain that the subject matter of new claims are fully enabled.

B) "Fragments"

The Examiner rejected claims that "recite in various forms nucleic acids comprising 'fragments' of a certain number of residues or encoding polypeptide fragments." Action at page 8. The Examiner alleged that "before the skilled artisan can make nucleotide sequences with additional flanking sequence, guidance

is required with respect to the identity of those flanking sequences." *Id.* Applicants respectfully traverse this basis for the rejection. The Examiner admitted that the specification provides guidance regarding certain B7RP1 fusion proteins, such as a fusion between the extracellular domain fragment of B7RP1 and the Fc region of IgG1. *Id.*, at page 9. However, the Examiner maintained that "[t]he scope of the instant claims encompasses *any* fragment and *any* additional sequences," and the cited B7RP1 fusion protein is only "a single example limited to a nucleic acid encoding a particular fragment of B7RP1...." *Id.* (emphasis original).

Applicants respectfully traverse and incorporate by reference the arguments made at page 21 of the Amendment and Response filed May 5, 2003. Solely to expedite prosecution and without acquiescing to any rejection, Applicants have added new claims 49-51 which include the language, "wherein the fragment has at least one activity selected from a T-cell proliferation activity, a T-cell activation activity, and a binding activity to CRP1."

Applicants assert that, in view of the specification, one skilled in the art would have been able to make the claimed fragments and to test the proteins which they encode for the ability to stimulate T-cell proliferation, to stimulate T-cell activation, or to bind to CRP1 without undue experimentation. As detailed previously, the specification describes a T-cell proliferation assay at Example 17, an in vitro T-cell stimulation assay at Example 21, and a binding assay between a CRP1 and a B7RP1 protein at Example 8. Even should the fragment contain additional flanking sequences (such as the B7RP1-Fc fusion protein described in the specification at page 29, line 27, to page 30, line 2, and Example 7), testing the resulting fusion protein for one of the enumerated activities was well within the guidance of the specification and the level of skill in the art.

Thus, the Examiner has failed to establish that the claims reciting the language "fragments" are not enabled by the specification.

C) "Hybridization"

The Examiner rejected claims that recite "hybridizes," because "[t]he fact that two nucleic acid sequences will hybridize under high stringency conditions does not in and of itself require that the two sequences encode proteins which share any functional activity." Action at page 9. The Examiner alleged that because "the instant hybridization language still does not require *a testable function* and limitations regarding both the hybridization *conditions* and thus does not allow the skilled artisan to make and use the hybridizing nucleic acids commensurate in scope with the instant claims without undue experimentation." *Id.* (emphasis original).

Applicants respectfully traverse and incorporate by reference the arguments made at page 22 of the Amendment and Response filed May 5, 2003. Solely to expedite prosecution and without acquiescing to any rejection, Applicants have added new claims wherein the hybridization language has been removed. Applicants therefore assert that this basis for the § 112, first paragraph (enablement), rejection is moot.

Applicants respectfully request reconsideration and withdrawal of the § 112, first paragraph, rejection based on enablement.

Rejections Under 35 U.S.C. § 102(a)

The Examiner rejected claims 2-4, 7, and 32-34 as allegedly "being anticipated by Ishikawa et al. (DNA Res. June 1998; 5:169-176, of record, see entire document) as evidenced by GenBank Accession No. AB014553 (released 06 Feb 1999, of record)." Action at page 11. The Examiner states:

> Ishikawa et al. teach KIAA0653, and that the sequence information for the cDNA of KIAA0653 is available under accession number AB014553.... KIAA0653 encompasses the entire nucleotide sequence set forth in SEQ ID NO: 11....KIAA0653 also encompasses the nucleic acid sequence as set forth in SEQ ID NO: 16 from approximately nucleotide 209 to 1098.

Id. Applicants respectfully traverse.

The sequences disclosed by GenBank Accession No. AB014553 (hereinafter "AB014553") are different from those of Applicants' invention. AB014553 discloses a 4,368 nucleotide mRNA sequence and

accompanying translated polypeptide sequence. The nucleotide sequence is identical to SEQ ID NO: 16 over nucleotides 1-1027 and 2166-2361 (corresponding to nucleotides 72-1099 and 1100-1294 of SEQ ID NO: 17), but lacks the N-terminal 71 nucleotides of SEQ ID NO: 16, and also contains a 2360-nucleotide insert between nucleotides 1099 and 1100 of SEQ ID NO: 16. While the nucleotide sequence of AB014553 is thus identical to SEQ ID NO: 11 from nucleotides 129-993 (corresponding to nucleotides 1-864 of SEQ ID NO: 11), the translated polypeptide disclosed by AB014553 differs significantly from those of SEQ ID NOs: 12 and 17.

Ishikawa describes the nucleotide sequence of AB014553 as having an open reading frame of 558 amino acid residues. *See* Ishikawa at page 173, Table 1. In fact, AB014553 teaches that the open reading frame corresponds to the region from nucleotide 1 through nucleotide 1676 of this mRNA sequence. This open reading frame, however, does not encode the polypeptide of either SEQ ID NO: 12 or SEQ ID NO: 17. SEQ ID NO: 12 sets forth a 288 amino acid polypeptide, and SEQ ID NO: 17 sets forth a 302 amino acid polypeptide, while AB014553 discloses a 588 amino acid polypeptide. The first amino acid of both SEQ ID NOs: 12 and 17 corresponds to amino acid 43 of the translated AB014553 sequence. While the translated AB014553 sequence may encompass the entirety of SEQ ID NO: 12, it also includes significantly more amino acid sequence both N- and C-terminal to the sequence set forth in SEQ ID NO: 12 – 42 extra amino acids at the N-terminus and 216 extra amino acids at the C-terminus. A similar situation exists with SEQ ID NO: 17: the polypeptide of AB014553 has 42 additional amino acids at the N-terminus of SEQ ID NO: 17 and is entirely different than SEQ ID NO: 17 after amino acid 300, due to the presence of the 2360-nucleotide insert. In short, AB014553 does not teach a polypeptide with the same, or even similar N- and C-termini as the polypeptides set forth in SEQ ID NOs: 12 and 17.

For a reference to anticipate it must disclose every element of the claim. *See Hybritech Inc. v. Monoclonal Antibodies, Inc.*, 802 F.2d 1367, 1379, 231 U.S.P.Q. 81, 90 (Fed. Cir. 1986). AB014553 does not disclose every element of new claims 41, 43, 45, 46, 47 and 48, and claims depending therefrom.

First, as discussed previously, AB014553 teaches a polypeptide which is significantly larger than the polypeptide of either SEQ ID NO: 12 or 17, and which has different N- and C-termini from those polypeptides. Second, neither Ishikawa nor AB014553 provide detailed structural information regarding the encoded polypeptide, and specifically do not teach the presence of a signal sequence from about amino acids 1-18, 1-19, 1-20, 1-21, 1-22, 1-24, or 1-28. One of ordinary skill in the art would not expect to find a signal sequence buried in the middle of a polypeptide; the signal sequences taught by Applicants correspond to the region of amino acids 43-71 of the translated amino acid sequence of AB014553. In fact, Ishikawa and AB014553 do not teach any domains or even fragments of the KIAA0653 protein whatsoever. Finally, neither AB014553 nor Ishikawa teach that the KIAA0653 protein has a T-cell proliferation activity, a T-cell activation activity, or a binding activity to CRP1. Therefore, Ishikawa and AB014553 do not anticipate claims 41, 43, 45, 46, 47 and 48, and claims depending therefrom.

Moreover, Claims 40, 42, 44 and 49-51, to the extent that such claims encompass the nucleotide sequence set forth in GenBank Accession No. AB140533, now recite "wherein the nucleotide sequence is not the nucleotide sequence as set forth in GenBank Accession No. AB140533" such that only the nucleotide sequence specifically set forth in GenBank Accession No. AB140533 is disclaimed.

Applicants respectfully request reconsideration and withdrawal of the § 102(a) rejection.

Rejections Under 35 U.S.C. § 102(b)

A) GenBank Accession No. R23544

The Examiner rejected claims 2, 4, 6, and 34 under 35 U.S.C. § 102(b) as allegedly being anticipated by GenBank Accession No. R23544. Action at page 12. To attempt to support that rejection, the Examiner pointed to certain regions of identity of that sequence with certain regions of SEQ ID NOs: 11 and 16. For a reference to anticipate it must disclose every element of the claim. The sequence of GenBank Accession No. R23544 does not disclose every element of any of claims 2, 4, 6, or 34.

Solely to expedite prosecution and without acquiescing to any of the Examiner's contentions, Applicants have added new claims 39-48 which are not anticipated by the disclosure of GenBank Accession No. R23544 because it fails to teach every element of any of the new claims. For example, GenBank Accession No. R23544 encodes a polypeptide fragment having fewer than 75 amino acid residues of SEQ ID NO: 7, and fewer than amino acid residues 28-288 of SEQ ID NO: 17, and fewer amino acids than in the extracellular domain of B7RP1 in SEQ ID NO:17. Moreover, Claims 49-51, to the extent that such claims encompass the nucleotide sequence set forth in GenBank Accession No. R23544, now recite "wherein the nucleotide sequence is not the nucleotide sequence as set forth in ... GenBank Accession No. R23544" such that only the nucleotide sequence specifically set forth in GenBank Accession No. R23544 is disclaimed. Therefore, GenBank Accession No. R23544 does not anticipate the claimed subject matter.

B) GenBank Accession No. AA510455

The Examiner rejected claims 2, 4, 6, and 34 under 35 U.S.C. § 102(b) as allegedly being anticipated by GenBank Accession No. AA510455. Action at page 13. To attempt to support that rejection, the Examiner pointed to certain regions of identity and homology of that sequence with certain regions of SEQ ID NO: 6. For a reference to anticipate it must disclose every element of the claim. *See Hybritech*, 802 F.2d at 1379. The sequence of GenBank Accession No. AA510455 does not disclose every element of any of claims 2, 4, 6, or 34.

Solely to expedite prosecution and without acquiescing to any of the Examiner's contentions, Applicants have added new claim 39 which is not anticipated by the disclosure of GenBank Accession No. R23544 because it fails to teach every element of the claim. For example, GenBank Accession No. AA510455 is not a nucleotide sequence as set forth in SEQ ID NO: 6, it does not encode the polypeptide corresponding to SEQ ID NO: 7 from residues 1-322 or 47-322, and it does not encode a polypeptide fragment of at least about 75 amino acids of SEQ ID NO: 7. Since the polypeptide encoded by the nucleic

acid molecule of claim 39 is not anticipated by GenBank Accession No. AA510455 for at least the reasons discussed, claims depending from claim 39 are likewise not anticipated.

Accession No. AA510455 encodes a protein which is 100% identical to SEQ ID NO: 7 over residues 1-39, or over residues 41-103. However, Accession No. AA510455 contains an extra nucleotide at position 218 of SEQ ID NO: 7, which means that the residues encoded by Accession No. AA510455 after residue 39 would not be identical to those of SEQ ID NO: 7 if transcription and translation were to proceed directly from the nucleotide sequence described in Accession No. AA510455. Therefore, Accession No. AA510455 does not comprise a nucleotide sequence encoding a fragment of 75 or more amino acid residues of SEQ ID NO:7, and does not anticipate claim 39 or claims depending therefrom.

Applicants respectfully request reconsideration and withdrawal of the § 102(b) rejection.

Rejections Under 35 U.S.C. § 103(a)

The Examiner rejected claims 5 and 6 under 35 U.S.C. § 103(a) as allegedly being unpatentable over Ishikawa in view of Linsley. See Action at page 14. Those claims recite a host cell comprising a nucleic acid molecule of claim 3, which the Examiner rejected as allegedly being anticipated by Ishikawa. The Examiner cited Linsley as allegedly showing certain additional elements of the rejected claims.

The subject matter of claim 3 is now recited in claims 52-54 and the subject matter of claims 5 and 6 is now recited in claims 56 and 57. For at least the reasons stated above, Ishikawa does not anticipate claims 52-54. Moreover, Linsley does not remedy the deficiencies of Ishikawa. Because the nucleic acid molecules of claims 52-54 are patentable over Ishikawa in view of Linsley, claims 56 and 57 are likewise patentable. Moreover, the Applicant need not address the Examiner's contentions with respect to other elements of those claims. By not addressing those contentions, the Applicant in no way acquiesces to those contentions.

## Conclusion

Applicants respectfully request reconsideration and reexamination of the application, and the timely allowance of the pending claims.

Respectfully submitted,

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